

**Figure 1:**

Query= INSP097\_pep  
(1446 letters)

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,039,285 sequences; 328,747,273 total letters

Searching.....done

	Score	E
Sequences producing significant alignments:	(bits)	Value
ref XP_132895.1  (XM_132895) similar to ovomacroglobulin, ovosta...	1583	0.0
ref XP_090334.2  (XM_090334) similar to ovostatin precursor - ch...	1542	0.0
emb CAA55385.1  (X78801) ovomacroglobulin, ovostatin [Gallus gal...	1206	0.0
sp P20740 OVOS_CHICK OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) >gi ...	1206	0.0
ref NP_036620.1  (NM_012488) alpha-2-macroglobulin [Rattus norve...	1019	0.0
ref NP_000005.1  (NM_000014) alpha 2 macroglobulin precursor [Ho...	1016	0.0
prf  1009174A macroglobulin alpha2 [Homo sapiens]	1001	0.0
pir  JC5143 alpha-macroglobulin precursor - guinea pig >gi 13040...	991	0.0
ref NP_002855.1  (NM_002864) pregnancy-zone protein; Pregnancy z...	989	0.0
gb AAB51432.1  (L63543) endodermin [Xenopus laevis]	977	0.0

**Figure 2:**

>emb|CAA55385.1| (X78801) ovomacroglobulin, ovostatin [Gallus gallus]

Length = 1454

Score = 1206 bits (3121), Expect = 0.0

Identities = 641/1459 (43%), Positives = 928/1459 (62%), Gaps = 34/1459 (2%)

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Query: 1   MWKIIHLGVFLFHL SLSQSPNLQYVLLIPSVLQEGSLDKACAQLFNLTESVVLTVSLNYG 60
          MW   L + L H + + P QYVL++P+VLQ S + C Q ENL +++ + V L Y
Sbjct: 1   MWLKFILAILLLHAAAGKEPEPQYVLMVPAVLQSDSPSQVCLQFFNLNQTISVRVVLEYD 60

Query: 61   EVQTKIFEENVGTGENFFKCISFEVPQARSDEPLAFITFSAGKATLNLEERRSVAIRSRENV 120
          + T IFE+N T N +C++F +P S LAFI+F+AKG T +L+ERRSV I + E+
Sbjct: 61   TINTTIFEKNTTTSNGLQCLNFMIPPVTSVSLAFISFTAKGTTFDLKERRSVMIWNMESF 120

Query: 121  VFVQTDKPTYKPGQKEKKTLSYINIIFIFISVSSDHPSACKNTLSYSQDPEGNRIQQWV 180
          VFVQTDKP YKPGQ + + + F F V +P L QDP+ NRI QW
Sbjct: 121  VFVQTDKPIYKPGQS---VMFRVVALDFNEKFPVQEMYF-----LIAVQDPQNNRIFQWQ 171

Query: 181  NEESVGGILQLSFQLISEPILGWYEITVEMLNEKPTYHSFSVEEYVLPKFQMTVDAPENI 240
          N S I+Q+ F L EPILG Y+I V + ++T HSF VEEYVLPKF +TV AP ++
Sbjct: 172  NVTSEINIVQIEFPLTEEPILGNYKIIVTKKSGERTSHSFLVEEYVLPKFDVTVTAPGSL 231

Query: 241  LVVDSEFKVNVCALYTYGEFVDGKVQLSVCRESTAYHSCAHLISSLCKNFTIQLGKDGCV 300
          V+DSE V +CA+YTYG+PV+GKVQLSVCR+ +Y C S +C++FT L DGC+
Sbjct: 232  TVMDSELTVKICAVYTYGQPVGKQVQLSVCRDFDSYGRCKK--SPVCQSFTKDLDTDGCL 289

Query: 301  SKFINTDAFEXNREGYWSFLKVHALVTE DGTGVQLTGSKYVYIDSSVVKISFENMDMSYK 360
          S +++ FE NR GY L V A+VTE LT ++ + I + + FEN+D Y+
Sbjct: 290  SHILSSKVFE LNRI GYKRNLDVKAIVTEKEQVCNLTATQSSISITQVMSSLOFENVDDHHR 349

Query: 361  QGLPYFGQIKLLNPDNSPIPNEVVQLHLKDKIVGNYYTTDVNGIAQFFLDTYTFTYPNITL 420
          +G+PYFGQIKL++ DNSPI N+V+QL + +K N+TTD+NGIA F +DT P ++L
Sbjct: 350  RGIPYFGQIKLVKDNSPISNKVIQLFVNKNKNTHTFTDINGIAPFSIDTSKIFDPELSL 409

Query: 421  KATYVRPKSCYLPSWLTPQYLDHFLVSRFYSRTNSFLKIVPEPKQLECNHQKVTVHYS 480
          KA Y C+ W+ P Y DA V R YS T+SF++I P K + C ++++TV+Y
Sbjct: 410  KALYKTS DQCHSEGWIEPSYPDASLSVQRLYSWTSSSFVRIEPLWKDMSCGQKRMITVYYI 469

Query: 481  LNSEAYEDDSNVKFFYLMMVKGAILLSGQKEIRNKA-WNGNFSFPLSISADLAPAAVLFV 539
          LN+E YE + V F+Y+ M KG I+L+G+ ++ +A NG F PL ++ +APA L V
Sbjct: 470  LNTEGYEHINIVNFYYVGMAGKIVLTGEIKVNIQADQNGTFMIPLVVNEKMAPALRLLV 529

```

Query: 540 YTLHPSGEIVADSVRFQVDKCFKHKVNIKFSNEQGLPGSNASLYLQAAPVLFCAVGAVDG 599  
Y LHP+ E+VADSVRF ++KCFK+KV ++FS +Q L SN SL ++AA FCA+ AVD  
Sbjct: 530 YMLHPAKELVADSVRFSIEKCFKNKVLQFSEKQMLTTSNVSLVIEAAANSFCAVRAVDK 589

Query: 600 NVLLKSEQQLSAESVSSL--TSSXYGYFYHGLNDDGKEDPCIPQORDMFYNGLYYTPVS 657  
++LLKSE +LSAE++ +L GY ++GLNL+D +DPC+ D+F+ GLYY P++  
Sbjct: 590 SMLLLKSETELSAETIYNLHPIQDLQGYIFNGLNLEDDPDQPCVSSDDIFHKGLYYRPLT 649

Query: 658 NYGDGDIYNIVRNMGKLVFTNLHYRKPEVCVMERRRLPLPKPLYLETENYGPMHVSPSRIA 717  
+ D+Y +R+MG+K FTN R+P VC R P +L H V +++  
Sbjct: 650 SGLGPDVYQFLRDMGMKFFFTNSKIRQPTVCT--RETVRPPSYFLNAGFTASTHHV--KLS 705

Query: 718 CRGENADYVEQAIQTVRTNFPETWMWDLVSVSDSSGSANLSFLIPDTITQWEASGFCVNG 777  
+ ++ I++T+R FPETW+WD++ ++S+G A++S+ IPDTIT+W+AS FCV  
Sbjct: 706 AEVAREERGKRHILETIREFFFPETWIWDIILINSTGKASVSYPDTITTEWKASAFCEE 765

Query: 778 DVGFGISSTTTLEVSQPFIEIASPFSVVQNEQFDLIVNAFSYLNTCVEISVQVEESQNY 837  
GFG+S TL QPFF+++ P+S++ E F + N F+YLN C++I+V + ES +Y  
Sbjct: 766 LAGFGMSVPATLTAFQPFFVDLTLPYSIIHGEDFLVRANVFNYLNHCIKINVLLLES LDY 825

Query: 838 EANINTWKINGSEVIQAGGRKTNITWIIPKGLGKVNIIVVAESKQSSACPNEGMEQQKLN 897  
+A + + + +G + A RK+ +W I PK G V ++ AE+ AC E + +++  
Sbjct: 826 QAKLISPEDDGC--VCAKIRKSYVWNIFPKGTGDVLFSAITAETNDDEACEEEALRNIRID 883

Query: 898 WKDTVVKSFVLEPEGIEKERTQSFLICTEGAKASKQGVLDLPNDVVEGSARGFFT VVGDI 957  
++DT +++ LVEPEGI +E TQ+FLIC + S+ +DLP +VVEGS R F+VVGDI  
Sbjct: 884 YRDTQIRALLVEPEGIRREETQNFLICMKDDVISQDVAIDLPTNVVEGS PRPSFSVVGDI 943

Query: 958 LGLAMQNL-VVLQMPYGGGEQNAALLASDTYVLDYLNKSTEQLTEEVQSKAFFLLSNGYQR 1016  
+G A+QN+ +LQMP+G GEQN L A + YVLDYL T QL+E+V+SK L +GYQ+  
Sbjct: 944 MGTAIQNVHQLLQMPFGNGEQNMVLFAPNIYVLDYLDKTRQLSEDVKS KTIGYLVSGYQK 1003

Query: 1017 QLSFKNSDGSYSVFWQQNQKGSIWLSALTFKTLERMKKFVFIDENVQKQTLIWLSSQKKT 1076  
QLS+K+ DGSYS F ++++G+ WL+A +K+ +F++ID+NVQ QTLIWL+++QKT  
Sbjct: 1004 QLSYKHPDGSYSTFGIRDKEGNTWLTA FVYKSFAEASRFIYIDDNVQAQTLIWLATKQKT 1063

Query: 1077 SGCFKNDGQLFNHAWEGGDEEDISLTAYVVGMMFFEAGLNSTFPALRNALFCLEAALDSGV 1136  
GCF++ G L N+A +GG E ++SL+AY+ EAG + + +RNA +CLE A + +  
Sbjct: 1064 DGCFQSTGILVNNAMKGGVENELSL SAYITIALLEAGHSMSHTVIRNAFYCLETASEKNI 1123

Query: 1137 TNGYNHAILAYAFALAGKEKQVESLLQTL DQSATKLNNVIYWERERKPKTEEFPSFIPWA 1196  
T+ Y A++AYAF LAGK + ES L+ L +SA +++ YWE+ ++ E+ +  
Sbjct: 1124 TDIYTQALVAYAFCLAGKAEICESFLRELQKSAKEVDGSKYWEQNQRSAPK-SHLLDHV 1182

Query: 1197 PSAQTEKSCYVLLAVI---SRKIPDLTYASKIVQWLAQQMNSHGGFSSNQVINVGLILIA 1253  
S E + YVLLA++ +R DLT AS IVQW+ +Q NS+GGF+S Q V L +A  
Sbjct: 1183 QSTDVEITSYVLLALLYKPNRSQEDLTAKASAIQWIIIRQQNSYGGFASMQDTVVALQALA 1242

Query: 1254 ICGEEGLFSKNQNTVTFSSEGSSEIQF--NGHNRLLVQRSEVTQAPGQYTVDVVEGRGCTF 1311  
G S QN + +S+ + E F N NRLL+Q++ + Q PG+Y++ V G GC  
Sbjct: 1243 AYGAATYNSVTQNVIKINSKNTFEKVFTVNNENRLLQLQTPLPQVPGKYSLTVNGTGCVL 1302

Query: 1312 IQATLKYNVLLPKKASGFSLSLIVKNYSLT-----VFDLTVNLKYTGIRNKSSMVVIDV 1366  
IQ L+YN+ LP+ A GFSLS++ N S FD+ + YTG R+ S+MV+IDV  
Sbjct: 1303 IQTALRYNIHLPEGAFGFSLSVQ-TSNASCPRDQPGKFIDIVLISSYTGKRSSSNMVIIDV 1361

Query: 1367 KMLSGFTPTMSSIEELENKGQVMKTEVKNDHVLFYLENVF-GRADSFTFSVEQSNLVFNI 1425  
KMLSGF P SS+++L + VM+ E K +HVL YL N+ R TFSVEQ +V +  
Sbjct: 1362 KMLSGFVPVKSSLDQLIDDHTVMQVEYKKNHVLLYLGNILOKRRKEVTFSVEQDFVVTHTP 1421

Query: 1426 QPAPGMVYDYIEKGRQATA 1444  
+PAP +YDYIE A A  
Sbjct: 1422 KPAPVQIYDYIETEEYAVA 1440

**Figure 3:**

```

1   ataacacacc taatgacatg taacacactg ggagatggct aaaatttaaa catgacttaa
61  actttaagaa tgactcagga aatactggca aaatctcctg catggatata tagtcccata
121 ctcggttcc ctgactagtg agaacgtctg ggctcctaga acactgacct gtatgtggat
181 ctagcagaca cggcatattg actttttctt catctcattg gatcatgatg tggaagataa
                                     m   w   k   i

241 tacatctggg tgtttttctc tttcatctgt ctctttctca gtctccaaac ttgcagtatg
    i   h   l   g   v   f   l   f   h   l   s   l   s   q   s   p   n   l   q   y

301 ttctgctgat tccttctggt ctacaagaag gctctttgga taaagcttgt gccagctttt
    v   l   l   i   p   s   v   l   q   e   g   s   l   d   k   a   c   a   q   l

361 ttaatctcac tgaatctggt gttttgacgg tctccctcaa ctatggtagag gtccagacca
    f   n   l   t   e   s   v   v   l   t   v   s   l   n   y   g   e   v   q   t

421 aaatatttga agaaaatggt actggagaaa atttcttcaa atgcatcagc tttgagggttc
    k   i   f   e   e   n   v   t   g   e   n   f   f   k   c   i   s   f   e   v

481 ctcaggccag atctgaccca ctggcattta ttacattttc tgctaaagga gccactctca
    p   q   a   r   s   d   p   l   a   f   i   t   f   s   a   k   g   a   t   l

541 acctggaaga gaggagatct gtggcaatca gatccagaga gaatgtggtc tttgtacaga
    n   l   e   e   r   r   s   v   a   i   r   s   r   e   n   v   v   f   v   q

601 ctgataaacc cacctacaag cctggacaga aagaaaaaaaa aaccttgagt tcatatatta
    t   d   k   p   t   y   k   p   g   q   k   e   k   k   t   l   s   s   y   i

661 acattatttt tatttttatt tcagtatcca gtgatcaccc ttcagcatgc aaaaatacac
    n   i   i   f   i   f   i   s   v   s   s   d   h   p   s   a   c   k   n   t

721 tttcttattc tcaggatcca gaaggcaatc gaatacaaca gtgggtgaat gaggagtctg
    l   s   y   s   q   d   p   e   g   n   r   i   q   q   w   v   n   e   e   s

781 tgggagggat tctacaactc tccttccagt taatctcaga gcccatcctc ggatggtatg
    v   g   g   i   l   q   l   s   f   q   l   i   s   e   p   i   l   g   w   y

841 aaatcacctg ggagatgctc aatgagaaga aaacatatca ctcttctctt gtggaagaat
    e   i   t   v   e   m   l   n   e   k   k   t   y   h   s   f   s   v   e   e

901 atgtgttacc caaatttcaa atgactgtgg atgcaccaga aaatatctta gttgtggact
    y   v   l   p   k   f   q   m   t   v   d   a   p   e   n   i   l   v   v   d

961 ctgaattcaa agtgaatgtc tgtgccttat atacctatgg tgaacctgtg gacgggaagg
    s   e   f   k   v   n   v   c   a   l   y   t   y   g   e   p   v   d   g   k

1021 tccaacttag tgtgtgcaga gaatctacgg cttatcattc atgtgctcat cttatcagtt
    v   q   l   s   v   c   r   e   s   t   a   y   h   s   c   a   h   l   i   s

1081 cactctgtaa aaattttacc attcagttgg ggaaagatgg ctgtgtctcc aagtttatta
    s   l   c   k   n   f   t   i   q   l   g   k   d   g   c   v   s   k   f   i

1141 acacagatgc ttttgagtta aatcggaag gatactggag tttcctcaaa gtgcatgtc
    n   t   d   a   f   e   l   n   r   e   g   y   w   s   f   l   k   v   h   a

1201 ttgttacaga ggacggaaca ggtgtgcagc ttacaggctc caagtacgta tacatagact
    l   v   t   e   d   g   t   g   v   q   l   t   g   s   k   y   v   y   i   d

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1261 catcagtggg gaagattagt ttgagaata tggatatgtc ctacaaacag ggactccctt  
s s v v k i s f e n m d m s y k q g l p

1321 attttggcca gattaaattg cttaatccag acaactctcc aatcccaaat gaagttgttc  
y f g q i k l l n p d n s p i p n e v v

1381 agttgcatct gaaggacaaa atcgtgggaa actacaccac agatgtaaat ggcacgctc  
q l h l k d k i v g n y t t d v n g i a

1441 agtttttctt ggacacatat acgtttacat acccaaatat cactttgaaa gccacatatg  
q f f l d t y t f t y p n i t l k a t y

1501 ttcgacctaa gagctgctat cttcccagct ggttgacgcc tcagtacttg gatgctcact  
v r p k s c y l p s w l t p q y l d a h

1561 tcttagtctc acgcttttac tcccgaacga acagcttcct gaagattgtt ccagaaccaa  
f l v s r f y s r t n s f l k i v p e p

1621 agcagcttga atgtaatcac cagaagggtg ttactgtgca ttactcccta aacagtgaag  
k q l e c n h q k v v t v h y s l n s e

1681 catatgagga tgattccaat gtaaagttct tctatttgat gatggtaaaa ggagctatct  
a y e d d s n v k f f y l m m v k g a i

1741 tactcagtg acaaaaggaa atcagaaaca aagcctggaa tggaaacttc tcgttcccac  
l l s g q k e i r n k a w n g n f s f p

1801 tcagcatcag tgctgatctg gctcctgcag cgcctcgtt tgtctacacc cttcacccca  
l s i s a d l a p a a v l f v y t l h p

1861 gtggggaaat tgtggctgac agtgtcagat tccaggttga caagtgttt aaacacaagg  
s g e i v a d s v r f q v d k c f k h k

1921 ttaacataaa gttctctaac gagcagggct tacctgggtc caatgctagt ctctatcttc  
v n i k f s n e q g l p g s n a s l y l

1981 aagcggcgcc tgtcttattc tgtgccctcg gggctgtgga tgggaacgct cttctactga  
q a a p v l f c a l g a v d g n v l l l

2041 aatctgaaca acagctgtca gctgaaagt taagctctct gacttcctcc cgtatgggtt  
k s e q q l s a e s v s s l t s s p y g

2101 atttctacca tggcctcaat cttgatgatg gcaaggaaga cccttgcat cctcagaggg  
y f y h g l n l d d g k e d p c i p q r

2161 atatgttcta caatggttta tattacacac ctgtaagcaa ctatggggat ggagatatct  
d m f y n g l y y t p v s n y g d g d i

2221 ataatatgtg caggaacatg ggtctcaaag tctttacca tctccattac cgaaaaccag  
y n i v r n m g l k v f t n l h y r k p

2281 aagtatgtgt gatggagaga aggctgccac tccctaagcc gctttatcta gaaacagaaa  
e v c v m e r r l p l p k p l y l e t e

2341 attatgggtc aatgcatagt gttccgtcta gaattgcatg tagaggggag aatgctgact  
n y g p m h s v p s r i a c r g e n a d

2401 atgtagaaca ggctataatt caaacagtaa gaacaaactt cccagagaca tggatgtggg  
y v e q a i i q t v r t n f p e t w m w

2461 acctcgtcag tgtcgattcc tcaggctctg ccaatctttc gttcctcatt cctgatacga  
d l v s v d s s g s a n l s f l i p d t

2521 taacccaatg ggaggcaagt ggcttttgtg tgaatggcga cggttgattt ggcatttcct  
i t q w e a s g f c v n g d v g f g i s

2581 ctacaaccac tctagaagtc tccaacctt tctttattga aattgcctca cccttttcgg  
s t t t l e v s q p f f i e i a s p f s

2641 ttgttcaaaa tgaacaattt gatttgattg tcaatgcctt cagctacctg aatacatgtg  
v v q n e q f d l i v n a f s y l n t c

2701 tagagatttc tgttcaagtg gaggagtctc agaattatga agcaaattt aatacctgga  
v e i s v q v e e s q n y e a n i n t w

2761 aaatcaatgg cagtgaggtt attcaagctg gagggaggaa aacaaacatc tggactatta  
k i n g s e v i q a g g r k t n i w t i

2821 tacctaagaa attgggtaaa gtgaatatca ctgtagttgc tgagtccaaa caaagcagtg  
i p k k l g k v n i t v v a e s k q s s

2881 cttgcccaaa tgaaggaatg gaggcagaaa agctaaaactg gaaagacact gtgggtcaaaa  
a c p n e g m e q q k l n w k d t v v k

2941 gcttcttagt agagcctgaa ggtattgaaa aggaaaggac ccagagtttc cttatctgta  
s f l v e p e g i e k e r t q s f l i c

3001 cagaaggtgc caaagcctcc aagcaggag ttttggactt gccaaatgat gtagtagaag  
t e g a k a s k q g v l d l p n d v v e

3061 ggtcagccag aggctttttc actgttgtgg gggatattct aggacttgcc atgcagaatc  
g s a r g f f t v v g d i l g l a m q n

3121 tggttgttct ccaaattgcc tatggaggtg gagagcagaa tgctgcccta ctagcatctg  
l v v l q m p y g g g e q n a a l l a s

3181 atacttatgt tctggactat ctgaaatcta ctgagcaact gacagaggaa gttcaatcta  
d t y v l d y l k s t e q l t e e v q s

3241 aggctttctt tctcttatct aatggttatc aaaggcaatt atctttcaaa aactctgatg  
k a f f l l s n g y q r q l s f k n s d

3301 gttcctatag tgtgttttgg cagcagaatc agaaaggaag catatggctc agtgctctta  
g s y s v f w q q n q k g s i w l s a l

3361 cttttaagac attggagaga atgaaaaaat ttgtattcat tgatgaaaat gttcaaaaac  
t f k t l e r m k k f v f i d e n v q k

3421 agaccttaat ctggctttca agccaacaga aaacaagcgg ctgctttaag aatgatggcc  
q t l i w l s s q q k t s g c f k n d g

3481 agcttttcaa ccacgcctgg gaggggtggag atgaagagga catttcactc actgcatatg  
q l f n h a w e g g d e e d i s l t a y

3541 ttgttgggat gttctttgaa gctgggctca attocacttt tctgtctcta cgaaacgcac  
v v g m f f e a g l n s t f p a l r n a

3601 tcttttgcct tgaagcggca ttggacagtg gtgtcactaa tggctacaat catgcaattc  
l f c l e a a l d s g v t n g y n h a i

3661 tagcttatgc ttttgccctta gctggaaaag agaagaaagt ggaatcttta ctccaaaccc  
l a y a f a l a g k e k q v e s l l q t

3721 tggatcaatc tgccacaaaa ctaaataatg tcatctactg ggaaagagaa aggaaaccca  
l d q s a t k l n n v i y w e r e r k p

3781 agacagaaga atttccatcc tttattccct gggcaccttc tgctcagact gagaagagtt  
k t e e f p s f i p w a p s a q t e k s

3841 gctatgtgct gttggctgtc atttcccgga aaattcctga cctcacctat gctagtaaga  
c y v l l a v i s r k i p d l t y a s k

3901 ttgtgcagt gcttgcccaa cagatgaatt cccatggagg cttttcttcc aaccaggtga  
i v q w l a q q m n s h g g f s s n q v

3961 ttaatgtagg cctgatatta atagcaatat gcggggaaga ggggctcttc tctaagaatc  
i n v g l i l i a i c g e e g l f s k n

4021 aaaacactgt caccttttagc agtgaaggat ccagtggagt ccagtttaac ggtcataacc  
q n t v t f s s e g s s e i q f n g h n

4081 gcctactggt ccaacgttca gaagtaacac aggcacctgg acaatacaca gtagatgtgg  
r l l v q r s e v t q a p g q y t v d v

4141 aaggacgagg ttgtacattt atccaggcca cccttaagta caatgtttctc ctacctaaga  
e g r g c t f i q a t l k y n v l l p k  
INSPO97-CP1

4201 aggcattctgg attttctctt tctttggaaa tagtaaagaa ctactctttg actgtttttg  
k a s g f s l s l e i v k n y s l t v f

4261 acctcacagt gaacctcaaa tacactggaa ttgcgaataa attcaattatg gctcatatag  
d l t v n l k y t g i r n k s s m v v i

4321 attgaaaaat gctatcaaga tttaccccag ccattgscatc catggaagag cttaaaadaca  
d v k m l s g f t p t m s s i e e l e n

4381 atggcccaat gatgaagact gaagtcagaa atgaccaggt tctttctctac ttggaaaatc  
k g q v m k t e v k n d h v l f y l e n

4441 ctttttccca agcagacagt ttcaactttt ctgttgagca gagaacett gtgttcaaga  
v f g r a d s f t f s v e q s n l v f n

4501 ttccagccagc cccagccagc atctacagatt actacgaaa aggtagccaa gcaacagcca  
i q p a p g m v y d y y e k g r q a t a  
INSPO97-CP2

4561 ttgcccataagg ttattgaatg tgggtgtttat atctaacatt ccttgagcta ctaaactttc  
m p

4621 caaaatcaac ctctgtcttc acagagtaaa caataaatgg cattactttg tgtttctggtt  
4681 tctttatccc atgatgtgtc ttctgactga acccattttc cagt

**xxx** = INSP097 predicted receptor binding domain.

→ Position and sense of PCR primers-



Position and sense of PCR primers 

**Figure 5:**

Molecule: pCR4-TOPO-INSP097-CP1/-CP2, 4369 bps DNA Circular

Type	Start	End	Name	Description
MARKER	205		M13R	M13 rev priming site
MARKER	243		T3	T3 priming site
REGION	295	706	Insert	INSP097-CP1/-CP2 PCR product
GENE	295	699	cds	INSP097 receptor binding domain cds
MARKER	295		CP1	INSP097-CP1 PCR primer
MARKER	706		CP2	INSP097-CP2 PCR primer
MARKER	759		T7	T7 priming site
MARKER	782		M13F	M13 for priming site
GENE	1571	2365	Kan	Kanamycin resistance gene ORF
GENE	2569	3429	Amp	Ampicillin resistance gene ORF
REGION	3574	4247	pUC ori	pUC origin

